

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:47:07 ; Search time 210.42 Seconds  
 (without alignments)  
 7.313 Million cell updates/sec

Title: US-09-331-631A-3\_COPY\_29\_73

Perfect score: 252

Sequence: 1 SEFDRQEVEECKRQCQLET..... RCVSQCDKRFEEIDWSKYD 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%, Listing first 45 summaries

Database : A\_Geneseq\_36:\*

1: /SIDS1/gcdata/geneseq/geneseq/AA1980.DAT:\*

2: /SIDS1/gcdata/geneseq/geneseq/AA1981.DAT:\*

3: /SIDS1/gcdata/geneseq/geneseq/AA1982.DAT:\*

4: /SIDS1/gcdata/geneseq/geneseq/AA1983.DAT:\*

5: /SIDS1/gcdata/geneseq/geneseq/AA1984.DAT:\*

6: /SIDS1/gcdata/geneseq/geneseq/AA1985.DAT:\*

7: /SIDS1/gcdata/geneseq/geneseq/AA1986.DAT:\*

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19: /SIDS1/gcdata/geneseq/geneseq/AA1998.DAT:\*

20: /SIDS1/gcdata/geneseq/geneseq/AA1999.DAT:\*

21: /SIDS1/gcdata/geneseq/geneseq/AA2000.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	252	100.0	666 19	W62828
2	252	100.0	666 19	Macadamia integrifolia
3	180	71.4	625 19	Macadamia integrifolia
4	78.5	31.2	590 19	Gossypium hirsutum
5	70.5	28.0	525 19	Theobroma cacao an
6	70.5	28.0	566 13	Sequence encoded by
7	67	26.6	218 19	Human TS1 protein
8	67	26.6	218 20	Thrombospondin I f
9	67	26.6	239 14	Human thrombospondin
10	67	26.6	441 19	Human concatameric
11	67	26.6	441 20	Thrombospondin I f
12	63	25.0	W90340	N-PSDD; V42310.

**RESULTS**

ID	W62828 standard: Protein; 666 AA.
XX	W62828;
XX	27-OCT-1998 (first entry)
XX	Macadamia integrifolia antimicrobial protein.
DE	antimicrobial protein; infestation; control.
KW	XX
OS	Macadamia integrifolia.
XX	
PH	Key
FT	Peptide
FT	Protein
FT	Location/Qualifiers
XX	1.28 /note= "signal peptide" 29.666 /note= "mature protein"
PN	W09827805-A1.
XX	PD 02-JUL-1998.
XX	PP 22-DEC-1997;
XX	PR 20-DEC-1996;
XX	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PA	XX
PI	Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
XX	WPI: 1998-37729/32.
DR	N-PSDD; V42310.
XX	G. max SBP1 protein
XX	G. max truncated S
XX	G. max SBP2 protein
XX	Membrane bound pro
XX	P. falciiparum Proj
XX	Plasmodium Proj
XX	P. falciparum Proj
XX	Plasmodium var-7.
XX	Sequence encoded b
XX	Zea mays antimicro
XX	Arabidopsis enhanc
XX	FBD-40 domain-in-contg
XX	Human cell signal
XX	Human beclin prote
XX	Antimicrobial maize
XX	A human beta-trans
XX	Arabidopsis FBP-
XX	F-box protein hbet
XX	Human cell signal
XX	Zea mays antimicro
XX	Maize Id gene NsII
XX	Maize Id protein.
XX	Arabidopsis Lat-
XX	Arabidopsis mutant
XX	Leech antiplatelet
XX	F-box protein FWD1
XX	Sequence gi/412661
XX	Acantho6. Ankylost
XX	Nematode extracted
XX	Adenovirus E1A ass
XX	Plasmodium DBL gen
XX	Extended human zsi





XX DT 18-AUG-1998 (first entry)  
 XX DE Human TSP1 protein.  
 XX KW TSPL; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;  
 XX KW liposome; DNA complex; tumour suppressor protein; treatment; neoplastic;  
 XX metabolic disease; tumour.  
 OS Homo sapiens.

FH Key Location/Qualifiers  
 FT Misc-difference 160  
 FT /note= "encoded by CGG"  
 FT Misc-difference 217  
 FT /note= "encoded by CT"  
 FT Peptide 12..27  
 FT /label= anti-angiogenic peptide  
 FT Peptide 142..159  
 FT /label= anti-angiogenic peptide  
 FT Peptide 199..217  
 FT /label= anti-angiogenic peptide  
 PN EP819758-A2.  
 XX PD 21-JAN-1998.  
 XX PP 16-JUL-1997; 97EP-0112154.  
 PR 16-JUL-1996; 96US-0680845.  
 PA (MIXS/)  
 PI Mixson AJ;  
 XX DR WPI; 1998-078839/08.  
 DR N-PSDB; V10493.  
 XX PT Complexes of DNA encoding anti-angiogenic peptide - with cationic  
 PT liposome(s) or cationic polymer, useful for, e.g. gene therapy of  
 tumours.  
 XX PS Claim 9; Page 6; 47pp; English.  
 CC This sequence represents the thrombospondin gene TSPL which is used  
 CC in a method to produce a cationic vehicle consisting of a cationic  
 CC liposome:DNA complex where the DNA encodes an anti-angiogenic peptide or  
 CC tumour suppressor protein. Such complexes are used for treatment of  
 CC neoplastic and metabolic diseases especially for gene therapy of tumours.  
 XX SQ Sequence 218 AA;

Query Match 26.6%; Score 67; DB 19; Length 218;  
 Best Local Similarity 39.5%; Pred. No. 0.49; Mismatches 15; Conservative 6; Indels 6; Gaps 2;

Oy 13 RQCMOLE----TSGQMRRC-VSQCDKREEDIDWSKY 44  
 | | | | : ||| | : ||||| : ||| :  
 Db 104 rscdslnnrcgssvqtrtchiqedkrfkqdgwshw 141

RESULT 8  
 Y06182 ID Y06182 standard; Protein; 218 AA.  
 AC Y06182;  
 XX DT 16-AUG-1999 (first entry)  
 XX DE Thrombospondin I fragment.  
 XX KW Anti-angiogenic; carrier:DNA complex; tumour; gene therapy; human;

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XX KW thrombospondin I; melanoma; lung cancer; colon cancer;  
 XX brain cancer; breast cancer.  
 XX OS Homo sapiens.

FH Key Location/Qualifiers  
 FT Misc-difference 160  
 FT /note= "encoded by CGG"  
 FT Misc-difference 161  
 FT /note= "encoded by CTC"  
 FT Misc-difference 162  
 FT /note= "encoded by TGC"  
 FT Misc-difference 163  
 FT /note= "encoded by AAC"  
 FT Misc-difference 177  
 FT /note= "encoded by GAA"  
 FT Misc-difference 178  
 FT /note= "encoded by GCG"  
 FT Misc-difference 179  
 FT /note= "encoded by CGG"  
 XX PN EP921193-A1.  
 XX PN 09-JUN-1999.  
 XX PP 07-JAN-1998; 98EP-0100135.  
 XX PR 05-DEC-1997; 97US-0985526.  
 PA (MIXS/)  
 PI Mixson AJ;  
 XX DR WPI; 1999-315406/27.  
 DR N-PSDB; X58725.  
 XX PT Inhibition of growth of solid tumors  
 XX PS Disclosure; Page 17-18; 46pp; English.  
 CC This sequence represents an anti-angiogenic fragment of the  
 CC thrombospondin I protein. The invention provides a carrier:DNA  
 CC complex that comprises DNA (see X58725-42) coding for an  
 CC anti-angiogenic protein or peptide, the complex being deliverable  
 CC to the site of a tumour *in vivo*, and which additionally comprises  
 CC regulatory elements for expressing the anti-angiogenic DNA in a  
 CC tumour or tumour vasculature. The complex may also include DNA  
 CC encoding a tumour suppressor protein, especially p53. The carrier  
 CC is a liposome, cationic polymer, micelle, microsphere, virus, viral  
 CC component, or a combination of these, and administration is by  
 CC intravenous or intratumoral injection. The complexes are useful in  
 CC gene therapy for inhibition of tumour growth. The types of tumors  
 CC which may be treated include solid tumors such as melanomas and  
 CC tumors in the lung, colon, brain and breast.

Query Match 26.6%; Score 67; DB 20; Length 218;  
 Best Local Similarity 39.5%; Pred. No. 0.49; Mismatches 15; Conservative 6; Indels 6; Gaps 2;

Oy 13 RQCMOLE----TSGQMRRC-VSQCDKREEDIDWSKY 44  
 | | | | : ||| | : ||||| : ||| :  
 Db 104 rscdslnnrcgssvqtrtchiqedkrfkqdgwshw 141

RESULT 9  
 R40823 ID R40823 standard; protein; 239 AA.  
 AC R40823;



FT Misc-difference 160  
 FT /note= "encoded by CGG"  
 FT 383  
 FT /note= "encoded by CGG"  
 XX PN EP921193-A1.  
 XX PD 09-JUN-1999.  
 XX PR 07-JAN-1998; 98EP-0100135.  
 XX PR 05-DEC-1997; 97US-0985526.  
 XX PA (MIXS/) MIXSON A J.  
 XX PI Mixson AJ;  
 XX DR WPI; 1999-315406/27.  
 XX N-PSDB; X58726.  
 PT Inhibition of growth of solid tumors  
 XX PS disclosure; Page 19-20; 46pp; English.  
 XX  
 CC The present sequence represents a concatamer of anti-angiogenic  
 CC fragments of thrombospondin I. The invention provides a carrier-DNA  
 CC complex that comprises DNA (see X58725-42) encoding at least one  
 CC anti-angiogenic protein or peptide, the complex being deliverable  
 CC to the site of a tumour in vivo, and additionally comprises  
 CC regulatory elements for expressing the anti-angiogenic DNA in a  
 CC tumour or tumour vasculature. The complex may also include DNA  
 CC encoding a tumour suppressor protein, especially p53. The carrier  
 CC is a liposome, cationic polymer, micelle, microsphere, virus, viral  
 CC intravenous or intratumoral injection, and administration is by  
 CC gene therapy for inhibition of tumour growth. The types of tumors  
 CC which may be treated include solid tumors such as melanomas and  
 CC tumors in the lung, colon, brain and breast. Use of concatamers  
 CC can increase the anti-angiogenic dosage level without altering the  
 CC amount of vector necessary for delivery.  
 SQ 441 AA;

Query Match 26 6%; Score 67; DB 20; Length 441;  
 Best Local Similarity 39.5%; Pred. No. 1;  
 Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

QY 13 ROCMQL---TSGOMRRC-VSGCDKREEDIWISKY 44  
 Db 104 rscdsslnnrcgsswqtrchiqecdkrkfqdgwshw 141

RESULT 12  
 ID W90340 standard; protein; 444 AA.  
 XX AC W90340;  
 XX DT 24-MAY-1999 (first entry)  
 DE G. max truncated SBP1 protein.  
 XX SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
 DE G. max truncated SBP1 protein.  
 XX SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
 KW seed; carbohydrate content; soybean.  
 XX Glycine max.  
 OS Glycine max.  
 PN WO953086-A1.  
 PD 26-NOV-1998.  
 PF 21-MAY-1998; 98WO-US10465.  
 PR 22-MAY-1997; 97US-0047568.  
 XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 XX Chao WS, Grimes HD;  
 PI Chao WS, Grimes HD;  
 DR WPI; 1999-070155/06.

XX 22-MAY-1997; 97US-0047568.  
 PR  
 XX  
 PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 XX  
 PI Chao WS, Grimes HD;  
 DR  
 XX WPI; 1999-070155/06.  
 PR  
 XX  
 PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 XX  
 PI Chao WS, Grimes HD;  
 DR  
 XX WPI; 1999-070155/06.

Query Match 25 0%; Score 63; DB 20; Length 444;  
 Best Local Similarity 38.2%; Pred. No. 3.3;  
 Matches 13; Conservative 4; Mismatches 15; Indels 2; Gaps 1;  
 ID W90339 standard; protein; 524 AA.  
 XX AC W90339;  
 XX DT 24-MAY-1999 (first entry)  
 XX DE G. max SBP1 protein.  
 XX SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
 DE G. max truncated SBP1 protein.  
 XX SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
 KW seed; carbohydrate content; soybean.  
 OS Glycine max.  
 PN WO953086-A1.  
 PD 26-NOV-1998.  
 PF 21-MAY-1998; 98WO-US10465.  
 PR 22-MAY-1997; 97US-0047568.  
 XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 XX Chao WS, Grimes HD;  
 PI Chao WS, Grimes HD;  
 DR WPI; 1999-070155/06.

modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any transgene in developing seeds.

CC seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any transgene in developing seeds.

XX Sequence 489 AA;

Query Match 24.8%; Score 62.5; DB 20; Length 489;  
Best Local Similarity 36.6%; Pred. No. 4.2;  
Matches 15; Conservative 3; Mismatches 14; Indels 9; Gaps 2;  
QY 7 EYECKERQCMOLE-TSGQMRRC(SQCD-----KRFED 38  
Db 38 elvtckhqcqgrgtyesdkrtclicqcdsmkerekqvee 78

Search completed: March 1, 2001, 15:47:07  
Job time: 232 sec